

The present invention provides a method for identifying one or more low abundance sequences differing by one or more single-base changes, insertions, or deletions, from a high abundance sequence in a plurality of target nucleotide sequences. The high abundance wild-type sequence is selectively removed using high fidelity polymerase chain reaction analog conversion, facilitated by optimal buffer conditions, to create a restriction endonuclease site in the high abundance wild-type gene, but not in the low abundance mutant gene. This allows for digestion of the high abundance DNA. Subsequently the low abundant mutant DNA is amplified and detected by the ligase detection reaction assay. The present invention also relates to a kit for carrying out this procedure.